

Replace the paragraph beginning at page 12, line 7, with the following rewritten paragraph:

--**Fig. 3.** DNA and protein sequence of streptokinase of *S. equisimilis* H46A (SEQ ID NOs:1 and 2, respectively) (GenBank accession number: gb/K02986/STRSKC).--

Replace the paragraph beginning at page 12, line 16, with the following rewritten paragraph:

--**Fig. 6.** DNA and protein sequence of the gene-segment encoding for FBDs 1-5 of human fibronectin (SEQ ID NOs:3 and 4, respectively) (the DNA sequence has been obtained from EMBL; the file and accession no.'s are ID-HSFIBI and X02761, K00799, K02273, X00307, X00739).--

Replace the paragraph beginning at page 12, line 32, with the following rewritten paragraph:

--**Fig. 11.** Nucleotide sequence of SK-NTRN gene (SEQ ID NO:5).--

Replace the paragraph beginning at page 12, line 34, with the following rewritten paragraph:

--**Fig. 12.** Predicted secondary structure of native (A) and translationally silently modified (B) 5'-ends of the SK gene sequence (SEQ ID NOs:27 and 28, respectively).--

Replace the paragraph beginning at page 13, line 7, with the following rewritten paragraph:

--**Fig. 14.** Nucleotide sequence of SK-NTR gene (SEQ ID NO:6).--

Replace the paragraph beginning at page 13, line 9, with the following rewritten paragraph:

--**Fig. 15.** Schematic depiction of the intergenic region of the chimeric SK-FBD(4,5) gene (above: SEQ ID NO:8; below: SEQ ID NO:7) highlighting the design of a gly-gly-gly sequence,

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a transglutaminase cross-linking site and several unique restriction enzyme sites wherein different inter-genic cassettes can be conveniently swapped into this region. Also shown is the location of the natural Bsm I site in the SK gene which was exploited as the common junction point for joining the FBD sequences to the SK gene.--

Replace the paragraph beginning at page 13, line 23, with the following rewritten paragraph:

--**Fig. 17b.** DNA sequencing data of SK-FBD(4,5) hybrid cassette in T7 expression vector, pET23(d) (SEQ ID NO:9).--

Replace the paragraph beginning at page 13, line 33, with the following rewritten paragraph:

--**Fig. 19b.** DNA sequencing data of SK-FBD(1,2) hybrid cassette in T7 expression vector (SEQ ID NO:10).--

Replace the paragraph beginning at page 14, line 4, with the following rewritten paragraph:

--**Fig. 21b.** DNA sequencing data of FBD(4,5)-SK gene block as present in the T7 expression vector pET23(d)-FBD(4,5)-SK (SEQ ID NO:11).--

Replace the paragraph beginning at page 14, line 10, with the following rewritten paragraph:

--**Fig. 22b.** DNA sequencing data of FBD(4,5)-SK-FBD(4,5) gene block as present in the T7 expression vector pET23(d)FBD(4,5)-SK-FBD(4,5) (SEQ ID NO:12).--

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Replace the paragraph beginning at page 29, line 10, with the following rewritten paragraph:

--RG-7 (forward primer)

5'-ATT GCT GGA CCT GAG TGG CT-3' (SEQ ID NO:25)

(specific for the first seven codons of the SK gene; Cf Fig. 11)--

Replace the paragraph beginning at page 29, line 15, with the following rewritten paragraph:

--RG-6 (reverse primer)

5'-TGG TTT TGA TTT TGG ACT-3' (SEQ ID NO:26)

(specific for codons 57-62 of SK gene)--

Replace the paragraph beginning at page 32, line 4, with the following rewritten paragraph:

--SCI-I

5'-C ATG ATA GCT GGT CCT GAA TGG CTA CTA GAT CGT CCT TCT GTA AAT
AAC AGC C-3' (SEQ ID NO:13)

(Partial NcoI site)--

Replace the paragraph beginning at page 32, line 10, with the following rewritten paragraph:

--SC-II

5'-AA TTG GCT GTT ATT TAC AGA AGG ACG ATC TAG TAG CCA TTC AGG
ACC AGC TAT-3' (SEQ ID NO:14)

(Partial MfeI site)--

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Replace the paragraph beginning at page 32, line 31, with the following rewritten paragraph:

--Mfe I primer: 5'-C-AGC-CAA-TTG-GTT-GTT-AGC-GTT-GCT-3' (SEQ ID NO:15)--

Replace the paragraph beginning at page 37, line 24, with the following rewritten paragraph:

--Forward primer (MY 13);

5'-CCG GAA TTC GCG CAA CAG ATT GTA CCC ATA GCT GAG AAG TGT TTT

Eco R1	Tansglutaminase- recognition sequence	hybridizes to upstream FBD(4,5) sequences
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GA-3' (SEQ ID NO:16)--

Replace the paragraph beginning at page 37, line 30, with the following rewritten paragraph:

--Reverse primer (MY 14);

5'-GGC CTT AAG AGC GCT CTA ACG AAC ATC GGT GAA GGG GCG TCT A-3'

(SEQ ID NO:17)

'clamp'	Afl II	Eco 47 III	stop codon	hybridizes to downstream FBD(4,5) sequences--
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Replace the paragraph beginning at page 38, line 27, with the following rewritten paragraph:

--The sequence of primer RG-3 is given below highlighting features incorporated in its design (bold letters denote non-hybridizing segments towards the 5'-end of the primer to distinguish these from the sequence complementary with respect to template DNA).

5'-G AAT GCT AGC TAC CAT TTA GCT GGT GGT GGC CAG GCG CAA CAG	
Bsm I Bst X Xcm I Bal I segment hybridizing with the	
(hybridizes to SK	5'-end of DNA block
gene at codons 376-383)	(-gly-gly-gly-) from PCR-1 at the TG
	recognition site

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ATT GTA CCC-3' (SEQ ID NO:18)--

Replace the paragraph beginning at page 45, line 1, with the following rewritten paragraph:

--Upstream primer, MY-10

SK sequence (codons 377-383; Cf. Fig. 3)

5'-G-TAC-GGA-TCC G-AAT-GCT-AGC-TAT-CAT-TTA-GCG-GGT-GGT-GGT-
 Bam HI Bsm I (gly-gly-gly-)

CAG-GCG-CAG-CAA-ATG-GTT-3' (SEQ ID NO:19)

hybridizes at the TG-recognitn. site just before the FBD sequences--

Replace the paragraph beginning at page 45, line 9, with the following rewritten paragraph:

--Downstream primer, MY-6

5'-GGC-CTT-AAG-AGC-GCT-CTA-TTA-GAT-GGT-ACA-GCT-TAT-TCT-3' (SEQ ID NO:20)

'clamp' Eco R1 Eco 47 II stop sequence hybridizing with FBD (1,2)
 site codons codons 99-104 (Cf.Fig.6)--

Replace the paragraph beginning at page 49, line 1, with the following rewritten paragraph:

--Upstream PCR-I primer KRG-8:

Transglutamate recognition site

_____ 150 152 154
 5'-CC-ATG-GTG-CAA-GCA-CAA-CAG-ATT-GTA-CCC-ATA-GCT-GAG-AAG-
 Partial Nco I hybridizes to beginning
 site of FBD(4) segment
 (codon numbers of FBD are
 shown as per Fig.6)

TGT-3' (SEQ ID NO:21)--

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Replace the paragraph beginning at page 49, line 9, with the following rewritten paragraph:

--Downstream PCR-I primer KRG-9:

sequence complementary to codons 1-5 of SK (No.'s indicated below)

5'-CTC-AGG-TCC-AGC-AAT-ACG-AAC-ATC-GGT-GAA-GGG-GCC-AGA-T-3'
 5 4 3 2 1 259 257 255 253
 (SEQ ID NO:22)

sequence hybridizing with end of FBD(5) segment
 (No.'s indicated are codons, as per Fig.6).--

Replace the paragraph beginning at page 49, line 21, with the following rewritten paragraph:

--Upstream PCR-II primer, KRG-11

FBD(5) sequence, as overhang;
 Codon numbers (cf. Fig.6)
 are indicated

sequence hybridizing with
 SK gene; codon No.'s (Cf.
 Fig.3) are indicated

5'-TTC-ACC-GAT-GTT-CGT - ATT-GCT-GGA-CCT-GAG-TGG-CTG-CTA-GAC-3'
 255 257 259 1 3 5 7 9
 (SEQ ID NO:23)--

Replace the paragraph beginning at page 49, line 29, with the following rewritten paragraph:

--Upstream PCR-II primer, KRG-12

5'-TGG-TTT-TGA-TTT-TGG-ACT-TAA-GCC-TTG-3' (SEQ ID NO:24)
 62 60 58 56 54

Note: sequence hybridizing with SK gene (codon No.'s are indicated; see Fig. 3)--

In the drawings:

Substitute the enclosed 26 sheets of formal drawings filed herewith for the original informal drawings as filed with the application.